VIREMIA AND IMMUNOGENICITY PROFILES OF MOLECULARLY-DERIVED LIVE-ATTENUATED MONOVALENT DENGUE VACCINES IN RHESUS MACAQUES

Mammen MP Jr, Nisalak A, Gettayacamin M, Markoff L, Eckels KH, Kelly EP, Narupiti S and Vaughn DW

Multiple approaches to a safe and effective tetravalent dengue vaccine are being pursued, to include genetically engineered live-attenuated virus vaccines. Viruses derived from infectious DNA clones (IC) of wild-type and cell-passaged dengue viruses (DENV) with and without site-specific mutations (mutant F, mutF) were administered to Rhesus macaques (*Macaca mulatta*) to study resultant viremia and immunogenicity profiles compared to homotypic wild-type virus and non-cloned primary dog kidney (PDK)-passaged live-attenuated vaccine viruses to identify vaccine candidates associated with reduced viremia and robust neutralizing antibody responses. Groups of five flavivirus-naïve monkeys were assigned to receive 1 of 8 dengue wild-type or vaccine viruses [DEN-1 WP (Parent, wild-type), DEN-1 WP mutF, DEN-1 45AZ5 PDK-20, DEN-1 45AZ5 PDK-20 IC, and DEN-1 45AZ5 PDK-20 mutF; and DEN-2 S16803 (wild type), DEN-2 S16803 PDK-50, and DEN-2 S16803 PDK-50 IC]. The viremia profiles for monkeys infected with DEN-1 mutF viruses and PDK-passaged viruses were comparable with lower viremia titers compared to monkeys infected with wildtype DEN-1 viruses derived from IC or from tissue culture. Neutralizing antibody titers elicited by DEN-1 mutF, PDK-passaged viruses and other IC viruses were comparable at study day 180 but were lower than that elicited by the respective wild-type viruses. In contrast, monkeys immunized with DEN2 viruses derived from ICs developed mean viral loads much lower than those induced by PDK-passaged vaccine. IC-derived DEN2 viruses also elicited lower titers of neutralizing antibodies compared to viruses derived by PDK-cell-passage. Detailed results of the study will be presented.

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ASSESSING THE PREVALENCE OF *SALMONELLA SPP., CAMPYLOBACTER SPP., ARCOBACTER SPP.* AND *ENTEROCOCCUS SPP.* IN RETAIL FOODS IN BANGKOK, THAILAND

Vindigni SM, Srijan A, Wongstitwilairoong B, Marcus R, Hadler J, Meek J, Heimer R, and Mason C

Worldwide, foodborne illness is often associated with consumption of meats and poultry products sold at retail markets. We conducted a cross-sectional retail food study in Bangkok, Thailand to assess the prevalence of bacterial pathogens on retail food samples. We purchased raw chicken, beef, pork and chicken eggs from fresh markets and supermarkets and tested them for *Salmonella spp.*, *Campylobacter spp.*, *Arcobacter spp.*, and *Enterococcus spp.* Suspect bacterial pathogens

were isolated by differential culture and serotyped. A total of 200 samples were collected from 50 markets between May and August 2003. Of the 200 samples tested, 121 (61%) were positive for at least one *Salmonella spp.* serogroup. A total of 175 *Salmonella spp.* were isolated. The most common serovar was *S.* Anatum followed by *S.* Corvallis and *S.* Derby. *Campylobacter spp*. was found in 31 (15.5%) of 200 samples. *C. jejuni* was isolated from 15% of fresh market chicken samples and 35% of supermarket chicken samples. *Arcobacter spp*. was isolated from 42 (21%) of the total specimens; fresh market chicken had significantly higher *A. butzleri* contamination than supermarket chicken. The presence of *Enterococcus spp*, an indication of fecal contamination, was detected in 188 (94%) samples, including 100% of the beef and pork sources. Few studies have examined retail food contamination in Thailand. In particular, the finding of large amounts of *Arcobacter spp*. on food warrants further study to determine pathogenicity.

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DETECTION OF *SHIGELLA* BY A PCR ASSAY TARGETING THE IPAH GENE SUGGESTS INCREASED PREVALENCE OF SHIGELLOSIS IN NHA TRANG, VIETNAM

Vu DT, Sethabutr O, Von Seidlein L, Tran VT, Do GC, Bui TC, Le HT, Lee H, Houng HS, Hale TL, Clemens JD, Mason C and Dang DT

Shigella spp. are exquisitely fastidious gram-negative organisms which frequently escape detection by traditional culture methods. To get a more complete understanding of the disease burden caused by *Shigella* in Nha Trang, Vietnam, real-time PCR was used to detect *Shigella* DNA. Randomly selected rectal swab specimens from 60 *Shigella* culture-positive patients and 500 *Shigella* culture-negative patients detected by population-based surveillance of patients seeking care for diarrhea were processed by real-time PCR. The target of the primer pair is the invasion plasmid antigen H gene sequence (*ipaH*), carried by all four *Shigella* species and enteroinvasive *Escherichia coli*. *Shigella* spp. could be isolated from the rectal swabs of 547 of 19,206 (3%) patients with diarrhea. *IpaH* was detected in 55 of 60 (93%) *Shigella* culture-positive specimens, whereas it was detected in 87 of 245 (36%) culture-negative patients free of dysentery ($P < 0.001$). The number of PCR cycles required to detect a PCR product was highest for culture-negative, nonbloody diarrheal specimens (mean number of cycles to detection, 36.6) and was lowest for children with culture-positive, bloody diarrheal specimens (mean number of cycles, 25.3) ($P < 0.001$). The data from real-time PCR amplification indicate that the culture-proven prevalence of *Shigella* among patients with diarrhea may underestimate the prevalence of *Shigella* infections. The clinical presentation of shigellosis may be directly related to the bacterial load.

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